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Surveillance of respiratory syncytial virus occurrences in Kenya from 2006-2010

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Background: RSV is the most common cause of severe lower respiratory disease in young infants. RSV infection causes both mild and serious respiratory diseases in older children and adults. Primary RSV infection predominantly arises in the first two years of life. In Kenya RSV is one of the leading cause of non influenza respiratory pathogen that affect children

Kenya National Influenza Centre (NIC) began screening for RSV in Oct 2006 as part of the ongoing surveillance of Human Influenza and other respiratory viruses.

The objective of this study was to determine the occurrences of RSV in Kenya

Methods: Nasopharyngeal swab specimens were collected from consenting patient's ≥ 2 months old presenting with fever (≥ 38°C) accompanied by cough and/or sore throat reported within 72 hours of onset of symptoms. Specimens were transported to the NIC where they were inoculated into Hep-2 cell line. RSV produces a characteristic CPE consisting of syncytia formation. After observing cells for Cytopathic effect, samples were analyzed by direct immunofluorescence assay (IFA).

Results: A total of 12769 samples of nasopharyngeal aspirates were collected between October 2006 and October 2010. Respiratory viruses were isolated in 2609 representing 20% of these samples. Notably, 317 (12%) of these were RSV. Out of the 317 isolates, 198 (63%) were from children <2years, 105 (33%) were from 2-5years and 14 (4%) were from > 5years of age. Our results indicate that in Kenya, 96% of RSV cases occur in children < 5years of age with children < 2years being the most affected.

Conclusion: This study emphasizes the importance of RSV surveillance and reinforces the need to diagnose these infections to provide epidemiological data that may be used to monitor the disease in Kenya. These findings also highlight the need to continue to improve respiratory virus detection assays in addition to RSV testing for the clinical diagnosis and community surveillance of respiratory viral infections in the country.

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Unique distribution of *emm* types and superantigen gene profiles of group A streptococci isolated in Thailand

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Background: *Streptococcus pyogenes* or group A streptococci (GAS) cause an array of invasive and non-invasive diseases and post-infectious sequelae such as rheumatic fever and acute glomerulonephritis. Data on GAS in Thailand are limited. The cell surface M protein encoded by the *emm* gene is a GAS virulence factor, and *emm* typing has been used as an epidemiological marker for GAS. We characterized GAS isolates in Thailand based on *emm* typing and superantigen gene profiling.

Methods: A total of 347 GAS isolates from 275 invasive, and 72 non-invasive cases in 57 provincial hospitals during 1994-2011 were tested. We examined the *emm* types by DNA sequencing and superantigen profiles by amplification of 9 *spe* genes, *smeZ*, and *ssa*.

Results: Sixty-seven *emm* types and 83 subtypes including 3 novel subtypes were identified. The 10 most prevalent *emm* types (in descending order) were 44, 81, 104, 22, 75, 25, 1-2, 58, 79, and st11014 in invasive isolates and 44, 1-2, st11014, 88, 25, 75, 109, 60, 63, and 76 in non-invasive isolates. The *emm*44 (10.9%) and *emm*1-2 (5.2%) were two of the most frequently observed overall. These types are also reported to be among the most common in Nepal and India, while *emm*22 (4.3%) predominates in China, Korea, Taiwan, Chile and Lebanon. st11014 (3.8%) was common in Thailand but has rarely been reported globally. The GAS isolates possessed various combinations of superantigen genes, but 54.0% of isolates fell into 10 profiles. Similar gene profiles were found among isolates of the *emm*1-2, 22, 104, 75, and st11014 types. *speA* was identified in only 9.8% of isolates, whereas *smeZ* (89.7%), *speG* (83.1%), *speH* (32.3%), *speJ* (28.6%), and *speM* (26.3%) were common. Invasive isolates more commonly possessed *speG*, *speI*, *speL*, *speM*, and *smeZ* genes (17.8-94.2%) than did non-invasive isolates (8.3-75.0%).

Conclusion: Overall, the *emm* types among invasive and non-invasive GAS isolates in Thailand have a distribution different from that in other areas of the world. Our findings have implications for proposed GAS vaccines targeting M proteins. Of 67 *emm* types found, only 20 were among those included in a 30-valent M protein vaccine under evaluation.

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